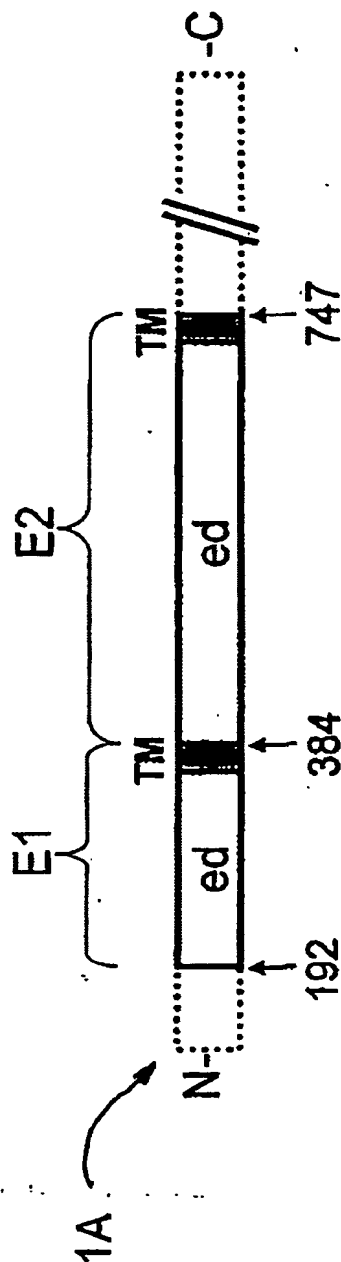


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TME1: 347-MIAGAHWGVLGIA<sup>U</sup>YFSMVGNWAKVLVLLLFAGVDA-383

\*\*\* \* \* \* \* \*\* \*\*\*\*\* \* \*

TME2: 717-EYVLLFLLLADARVCCLWMLLISQAEA-746

\*\*\*\*\* \* \* \*\*\*\*\* \* \*

FIG. 1

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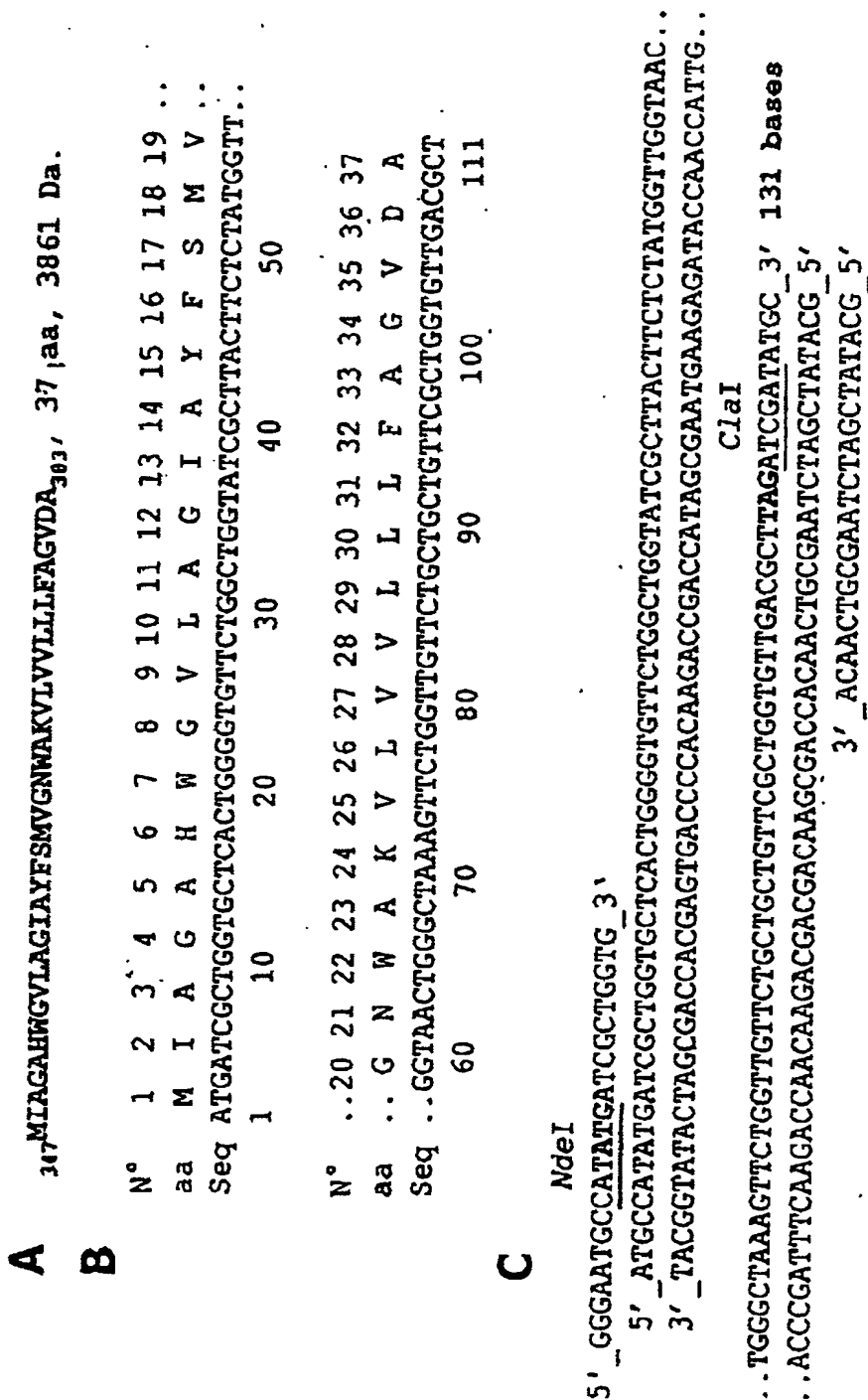


FIG. 2

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**D**

OL11(+): 5'atgccatatgatcgctgctcactggggtgtctggctggtatcgcttacttctctatggttgtaactggg  
OL12(-): 5'gcataatcgatctaagcgtaacacacagcgacagcagcagagaacacagaaactttagccagttaccaaccatagagaa

Cloning in pT7-7:

OL13(+): 5'gggaatgccatatgatcgctgggtg  
OL14(-): 5'gcataatcgatctaagcgtaacaa

Cloning in pGEXKT:

OL15(+): 5'ggatccatggaatacgtgttgc (without DP site)  
OL17(+): 5'ggatccgaacccgatggaatacgtgttgc (with DP site)  
OL16(-): 5'gaattcctaagcttcagcctgag

Cloning in pET32a:

OL18(+): 5'gtgatatctgatctgtctggtggtgt (hybridizes to the segment 915-932 of pGEXKT)  
OL16(-): 5'gaattcctaagccttcagcctgag

Cloning in pT7-7 of (M)DP-TME1::

OL19 (+) : 5'- CGCATATGGACCCGATCGCTGGTGCT -3' (Nde I underlined)  
OL20 (-) : 5'-GAATTCCTAAGCGTCAACACCAGC-3' (EcoR I underlined)

FIG. 2

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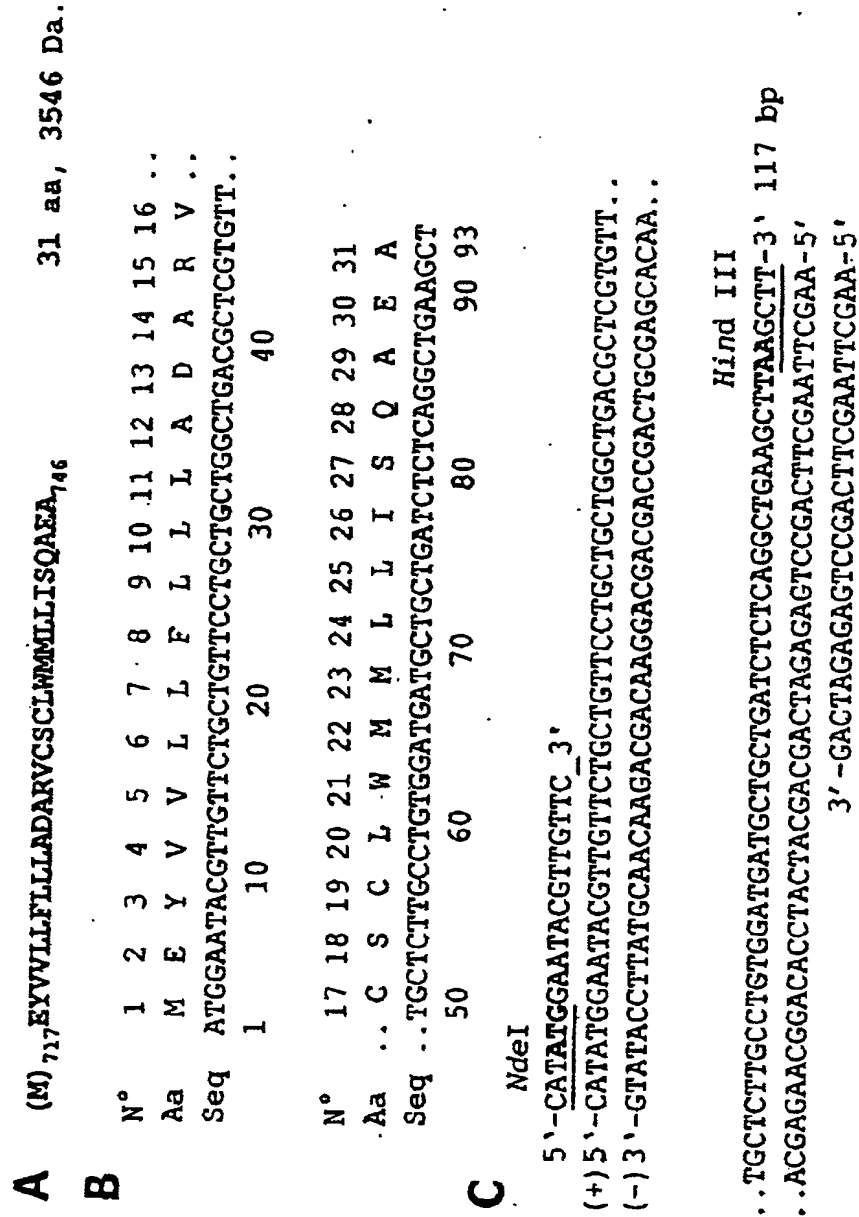


FIG. 3

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D

OL21(+): 5'catatgaatacgttggttctgctgttcctgctgctgctgacgctcgtgttgctctcttgccctgtggat  
OL22(-): 5'aagcttaagcttcagcctgagagatcagcagcatcatccacaggcaagagcaaacac

Cloning in pT7-7:

OL23(+): 5'catatgaatacgttggttc  
OL24(-): 5'aagcttaagcttcagcctgagagatcag

Cloning in pGEXKT:

OL25(+): 5'ggaaccgaatacgttggttc (without DP site)  
OL27(+): 5'ggaaccgaacccggaatacgttggttc (with DP site)  
OL26(-): 5'gaattcttaagcttcagcctgagagatcag

Cloning in pET32a:

OL18(+): 5'gtgatatctgatctgtctgtggtggt (hybridizes to the segment 915-932 of pGEXKT)  
OL26(-): 5'gaattcttaagcttcagcctgagagatcag

Cloning in pT7-7 of (M)DP-TME2:

OL28 (+) : 5'- CGCATATGACCCGGAATACGTTGTTC-3' (Nde I underlined)  
OL29 (-) : 5'-CAGAATTCCTAAAGCTTCAGCCTGAGAG-3' (EcoR I underlined)

FIG. 3

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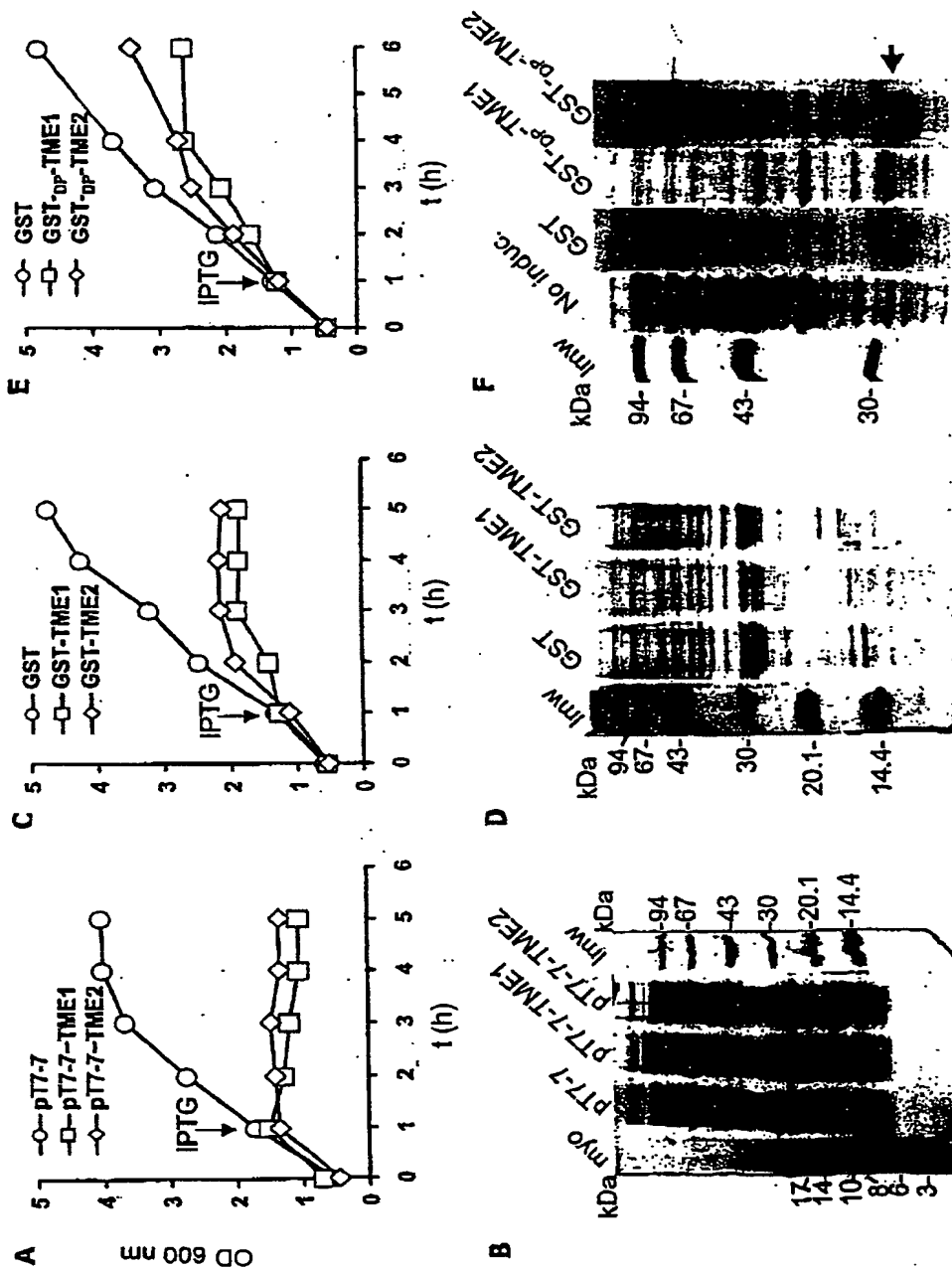


FIG. 4

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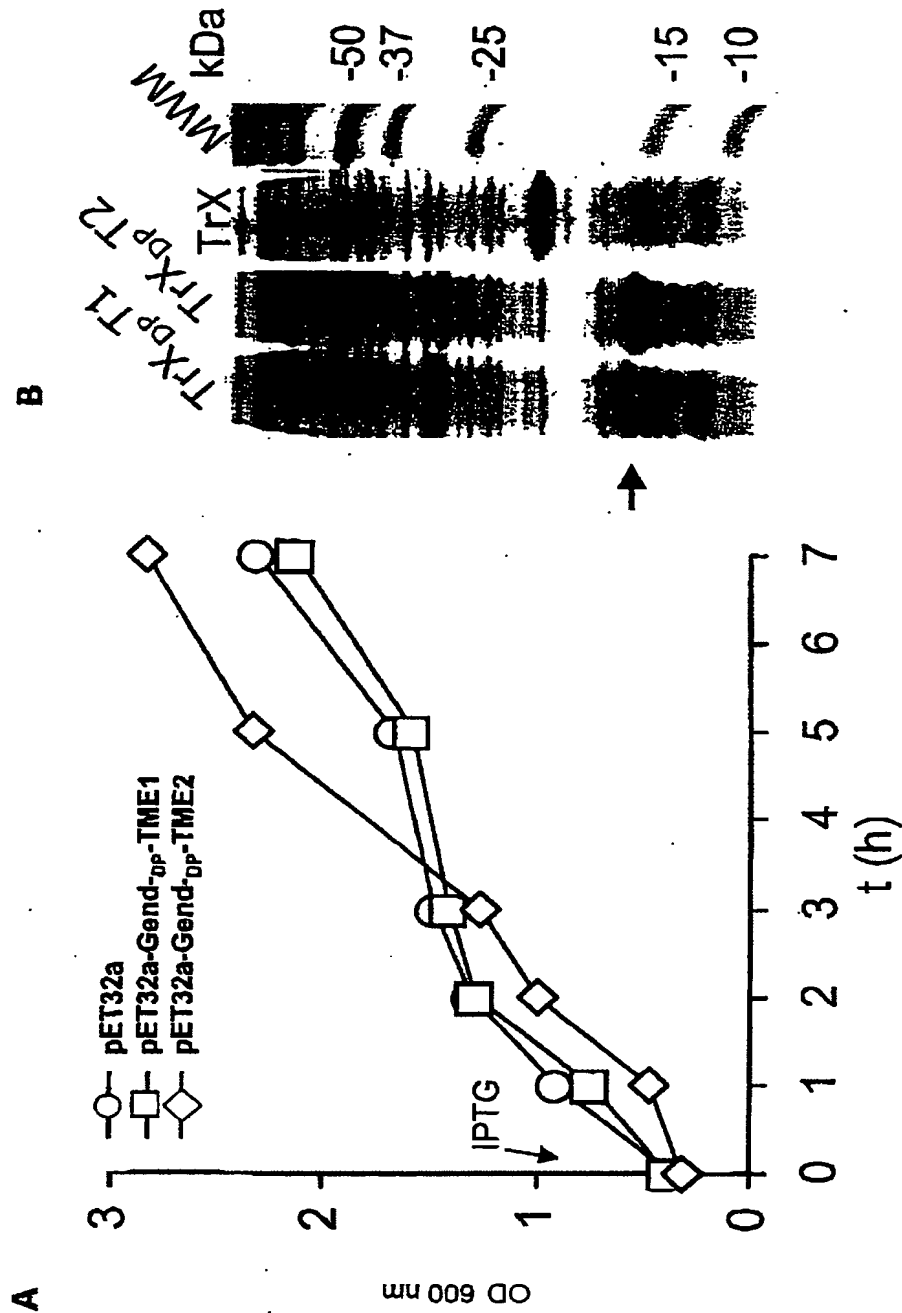


FIG. 5

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GST :  
 MSPILGYWKIKGLVQPTRLLEYLEEKYEHL YERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIRIYA  
 ADKHNMLGGCPKERAESI MLEGAVLDIRYGVSR IAYSKDFETLVDFLSKLPMLKMFEDRLCHKTYLNGDHVTH  
 PDFWLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGSDHPPKSDLSGGG  
GGLVPRGS/PGIHRD

GST-TME2 :  
 MSPILGYWKIKGLVQPTRLLEYLEEKYEHL YERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIRIYA  
 DKHNMLGGCPKERAESI MLEGAVLDIRYGVSR IAYSKDFETLVDFLSKLPMLKMFEDRLCHKTYLNGDHVTHPD  
 FMYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGSDHPPKSDLSGGGGGL  
VPRGS/EYVLLFIILADARVCSLWMLLISQAEA

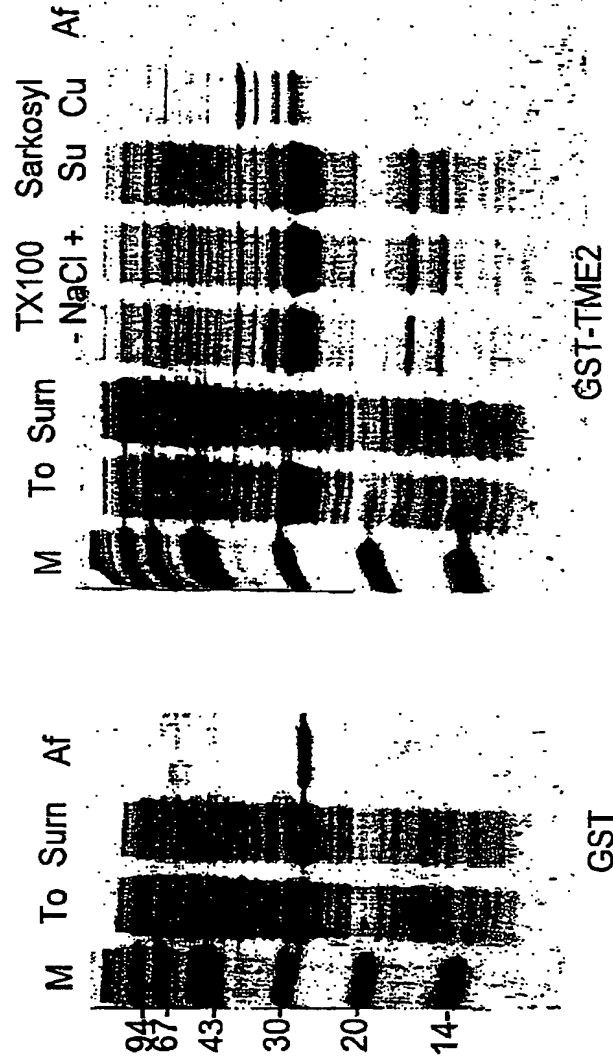


FIG. 6



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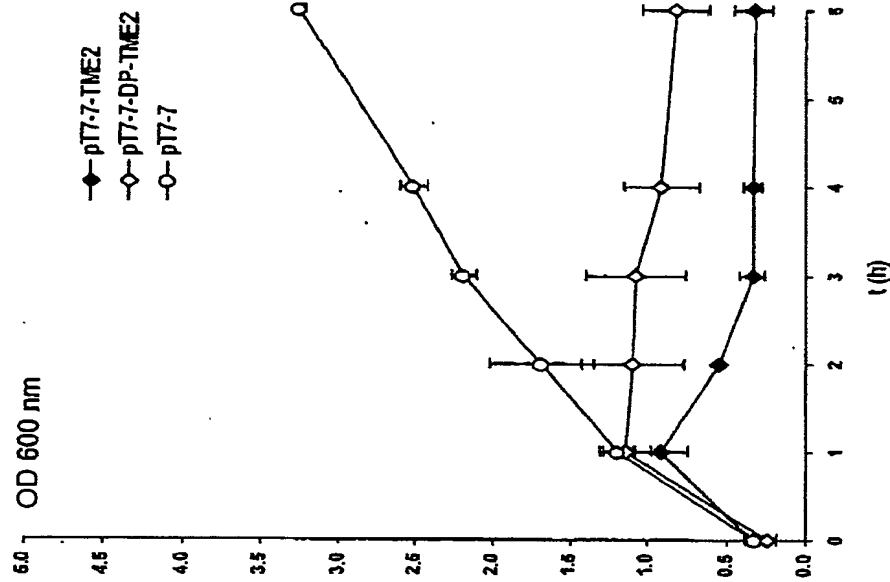


FIG. 7B

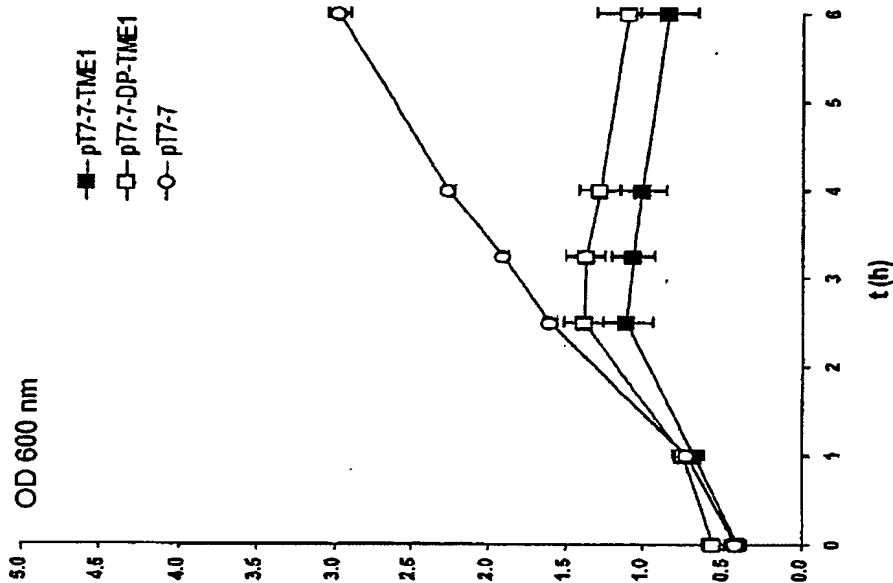


FIG. 7A